

SEQUENCE LISTING

<110> National Food Research Institute
<120> Erythrose Reductase, its cDNA and cell which the cDNA express
<130> P131238K
<160> 7

<210> 1

<211> 1119

<212> DNA

<213> Trichosporonoides megachiliensis

<400> 1

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gcc ctt gga ttt ggt act tgg caa gct gaa cct ggt caa gtg ggt gca 96
Ala Leu Gly Phe Gly Thr Trp Gln Ala Glu Pro Gly Gln Val Gly Ala
20 25 30

agt gtc aag aac gct gtc aag gct ggg tac cgt cat ttg gat ttg gcc 144
Ser Val Lys Asn Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala
35 40 45

aaa gtg tac caa aac caa tcg gaa att gga gta gca ctt cag gaa ctg 192
Lys Val Tyr Gln Asn Gln Ser Glu Ile Gly Val Ala Leu Gln Glu Leu
50 55 60

ttt gat caa ggt att gtt aaa cgg gaa gat ttg ttt att acg tcc aaa 240
Phe Asp Gln Gly Ile Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys
65 70 75 80

gta tgg aat aac cgt cat gct cct gaa cat gtt gag cct gca ttg gac 288
Val Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp
85 90 95

gaa aca ttg aaa gaa ctt gga ttg tcc tac ttg gat ttg tac ttg att			336
Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile			
100	105	110	
cat tgg ccc gtt gcg ttc aag ttt act acg cct caa gaa cta ttc cct			384
His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Gln Glu Leu Phe Pro			
115	120	125	
act gag ccg gat aac aag gaa ttg gcc gcg att gat gat tca atc aag			432
Thr Glu Pro Asp Asn Lys Glu Leu Ala Ala Ile Asp Asp Ser Ile Lys			
130	135	140	
ttg gta gac act tgg aag gca gtt gta gca ctc aaa aaa acg ggt aag			480
Leu Val Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys			
145	150	155	160
acc aaa tcc gtt ggt gtg tcg aac ttc act acg gat ttg gta gac ttg			528
Thr Lys Ser Val Gly Val Ser Asn Phe Thr Thr Asp Leu Val Asp Leu			
165	170	175	
gtt gaa aaa gcg tcg ggg gaa cga ccg gcg gtc aat cag att gaa gca			576
Val Glu Lys Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala			
180	185	190	
cac cca ttg tta caa cag gat gaa ttg gtt gct cat cac aag agt aaa			624
His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys			
195	200	205	
aac att gtg att act gcg tac agt cct ttg gga aac aat gtg agt ggg			672
Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ser Gly			
210	215	220	
aaa cca cct ctg act caa aac cct ggg att gaa gca act gcg aaa cgg			720
Lys Pro Pro Leu Thr Gln Asn Pro Gly Ile Glu Ala Thr Ala Lys Arg			
225	230	235	240
tta aat cat act cct gct gcg gtc ttg ctt gca tgg ggg att caa cgt			768

Leu Asn His Thr Pro Ala Ala Val Leu Leu Ala Trp Gly Ile Gln Arg
245 250 255
gga tac agt gta ttg gtc aag agt gtt aca cct tct cga att gag agc 816
Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Glu Ser
260 265 270
aat tat gat cag att acc ctt tct cct gaa gaa ttc cag aag gtt acg 864
Asn Tyr Asp Gln Ile Thr Leu Ser Pro Glu Glu Phe Gln Lys Val Thr
275 280 285
gat ttg atc aag gaa tat ggc gaa agt cgc aac aat att ccg ttg aat 912
Asp Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Ile Pro Leu Asn
290 295 300
tat aaa cct tca tgg ccc atc agt gtg ttt ggt aca tcg gat gaa gct 960
Tyr Lys Pro Ser Trp Pro Ile Ser Val Phe Gly Thr Ser Asp Glu Ala
305 310 315 320
aag gct act cat aag att aac acc aac ctt tga gttcagttt ggaactattt 1013
Lys Ala Thr His Lys Ile Asn Thr Asn Leu Stop
325 330
aaagctgctt gctggtcaca ttattgtcag tacctaccat gaagaattca atattatttt 1073
acattgtcaa ccattacatg gatccaaaaa aaaaaaaaaa aaaaaaa 1119

<210> 2

<211> 1077

<212> DNA

<213> Trichosporonoides megachiliensis

<400> 2

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gct ctt ggg tac ggt acc tgg caa gca gaa cct ggt cag gtc ggt gaa				96
Ala	Leu	Gly	Tyr	Gly
Trp	Gln	Ala	Glu	Pro
Gly	Gln	Val	Gly	Glu
20	25	30		
ggt gtc aag ctc gct gtt aag gct ggc tac cgt cat ttg gac ttg gcc				144
Gly	Val	Lys	Leu	Ala
Val	Lys	Ala	Gly	Tyr
Arg	His	Leu	Asp	Leu
Ala				
35	40	45		
aaa gta tac cag aac caa acc gag att ggc caa gct ctc aag gaa ctg				192
Lys	Val	Tyr	Gln	Asn
Gln	Thr	Glu	Ile	Gly
Gln	Ala	Leu	Lys	Glu
Leu				
50	55	60		
ttt gat gag ggt gtt gtc aag cgt gag gac ctt ttc atc act tcc aag				240
Phe	Asp	Glu	Gly	Val
Val	Lys	Arg	Glu	Asp
Leu	Phe	Ile	Thr	Ser
Lys				
65	70	75	80	
ctt tgg aac aac cgc cac gct cct gag cac gtt gag cct gcg ctc gac				288
Leu	Trp	Asn	Asn	Arg
Asn	His	Ala	Pro	Glu
His	Val	Glu	Pro	Ala
Leu	Asp			
85	90	95		
gag act ctt aag gag ttg ggt cta tcc tat ttg gac ctg tac ttg att				336
Glu	Thr	Leu	Lys	Glu
Leu	Gly	Leu	Ser	Tyr
Leu	Asp	Tyr	Leu	Tyr
Ile				
100	105	110		
cac tgg cct gtt gct ttc aag ttc act act ccc gat gaa ctg ctt cct				384
His	Trp	Pro	Val	Ala
Phe	Lys	Phe	Thr	Thr
Thr	Pro	Asp	Glu	Leu
Pro	Leu			
115	120	125		
gct gac cct acc aac aag gac ctt gcc tac att gac gat tcg gtc aaa				432
Ala	Asp	Pro	Thr	Asn
Lys	Asp	Leu	Ala	Tyr
Ile	Asp	Asp	Ser	Val
Lys				
130	135	140		
ttg tcc gac acc tgg aag gcg gtc gtc gcc ctg aaa aag acg ggt aag				480
Leu	Ser	Asp	Thr	Trp
Lys	Ala	Val	Val	Ala
Ala	Lys	Lys	Thr	Gly
Lys				
145	150	155	160	

acc aag tcg gtt ggt gtt tcg aac ttc agc act cgt ctg gtc gac ttg 528
 Thr Lys Ser Val Gly Val Ser Asn Phe Ser Thr Arg Leu Val Asp Leu
 165 170 175
 gtt gag gaa gct tcg ggc gaa cgt cct gcg gtt aac cag atc gaa gct 576
 Val Glu Glu Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala
 180 185 190
 cac ccc ttg ttg caa caa gac gag ttg gtt gct cac cat aag agc aag 624
 His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys
 195 200 205
 aac att gtc atc act gct tac agt ccc ttg ggc aac aat gtc gct ggt 672
 Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ala Gly
 210 215 220
 aaa cca cct ctg act gag aat ccc ggt att gtg gat gct gct aag cgt 720
 Lys Pro Pro Leu Thr Glu Asn Pro Gly Ile Val Asp Ala Ala Lys Arg
 225 230 235 240
 ctg aac cat act cct gct gct gtg ctc att gct tgg ggt att caa cgc 768
 Leu Asn His Thr Pro Ala Ala Val Leu Ile Ala Trp Gly Ile Gln Arg
 245 250 255
 ggg tac agc gtc ttg gtc aag tca gtt aca ccc tca cgg att aag agt 816
 Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Lys Ser
 260 265 270
 aac ttt gaa cag atc act ctg tct gat gag gaa ttc caa cgg gtt acc 864
 Asn Phe Glu Gln Ile Thr Leu Ser Asp Glu Glu Phe Gln Arg Val Thr
 275 280 285
 aac ctc atc aag gag tac ggt gag agc cgt aac aac gtt cct ttc aac 912
 Asn Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Val Pro Phe Asn
 290 295 300
 tac aag cct tcg tgg tct att gac gtc ttt ggt acc cag tac gag gct 960

Tyr Lys Pro Ser Trp Ser Ile Asp Val Phe Gly Thr Gln Tyr Glu Ala
 305 310 315 320
 aag gct acc cac aag att aac gct taa tgtgctctta tacaaaaaagt 1007
 Lys Ala Thr His Lys Ile Asn Ala Stop
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<210> 3
 <211> 1121
 <212> DNA
 <213> Trichosporonoides megachiliensis

<400> 3
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 gcc ctt ggc tac ggt acc tgg caa gca gaa cct ggt cag gtc ggt gaa 96
 Ala Leu Gly Tyr Thr Trp Gln Ala Glu Pro Gly Gln Val Gly Glu
 20 25 30
 ggt gtc aag ctc gct gtc aaa gct ggc tac cgt cac ttg gac ttg gcc 144
 Gly Val Lys Leu Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala
 35 40 45
 aaa gtt tac cag aac caa acc gag att ggc caa gct ctc aag gaa ctg 192
 Lys Val Tyr Gln Asn Gln Thr Glu Ile Gly Gln Ala Leu Lys Glu Leu
 50 55 60
 ttt gat gag ggt gtt gtc aag cgt gag gac ctt ttc atc act tcc aag 240
 Phe Asp Glu Gly Val Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys

65	70	75	80	
ctt tgg aac aac cgc cac gct cct gag cac gtt gag cct gcg ctc gac				288
Leu Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp				
85	90		95	
gag act ctt aag gag ctg ggt cta tcc tat ctg gac ctg tac ttg att				336
Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile				
100	105		110	
cac tgg cct gtt gct ttc aag ttc act act ccc gat gaa ttg ctc cct				384
His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Asp Glu Leu Leu Pro				
115	120		125	
gct gac cct acc aac aag gat ctt gcc tac gtt gac gat tcg gta aaa				432
Ala Asp Pro Thr Asn Lys Asp Leu Ala Tyr Val Asp Asp Ser Val Lys				
130	135		140	
ttg tcc gac acc tgg aag gcg gtc gtc gcc ctg aag aag acg ggt aag				480
Leu Ser Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys				
145	150	155	160	
acc aag tcg gtt ggt gtt tcg aac ttc agc act cgt ctg gtc gac ttg				528
Thr Lys Ser Val Gly Val Ser Asn Phe Ser Thr Arg Leu Val Asp Leu				
165	170		175	
gtt gag gaa gct tcg ggc gaa cgt cct gcg gta aac cag atc gaa gct				576
Val Glu Glu Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala				
180	185		190	
cac ccc ttg ttg caa caa gac gag ttg gtt gct cac cat aag agc aag				624
His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys				
195	200		205	
aac att gtc atc act gct tac agt ccc ttg ggc aac aat gtc gct ggt				672
Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ala Gly				
210	215		220	

aaa cca cct ctg act gag aac ccc ggt att gtg gat gct gct aag cgt 720
 Lys Pro Pro Leu Thr Glu Asn Pro Gly Ile Val Asp Ala Ala Lys Arg
 225 230 235 240
 ttg aac cat act cct gct gct gtg ctc att gct tgg ggt att caa cgc 768
 Leu Asn His Thr Pro Ala Ala Val Leu Ile Ala Trp Gly Ile Gln Arg
 245 250 255
 ggg tac agc gtc ttg gtc aag tca gtt aca ccc tca cgg atc aag agt 816
 Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Lys Ser
 260 265 270
 aac ttt gaa cag atc act ctg tct gat gag gaa ttc caa cgg gtt acc 864
 Asn Phe Glu Gln Ile Thr Leu Ser Asp Glu Glu Phe Gln Arg Val Thr
 275 280 285
 aac ctc atc aag gag tac ggt gag agc cgt aac aac gtt cct ttc aat 912
 Asn Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Val Pro Phe Asn
 290 295 300
 tac aag cct tcg tgg tcc att gac gtc ttt ggt acc cag gac gag gct 960
 Tyr Lys Pro Ser Trp Ser Ile Asp Val Phe Gly Thr Gln Asp Glu Ala
 305 310 315 320
 aag gct acc cac aag att aac gct taa tgtgctctta tacaaaaaagt 1007
 Lys Ala Thr His Lys Ile Asn Ala Stop
 325
 cgtttgaacc tgtaatgtgt gaatgttatac ctcattgttg catcgctctca tcaaaaaaaaaa 1067
 aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaa 1121

<210> 4

<211>

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed nucleotide based on erythrose reductase type III
DNA sequence

<220>

<221> unsure

<222> 9

<223> n=a or c or g or t

<400> 4

cargarctnt tygaycaygg 20

<210> 5

<211>

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed nucleotide based on erythrose reductase type III
DNA sequence

<220>

<221> unsure

<222> 3

<223> n=a or c or g or t

<220>

<221> unsure

<222> 18

<223> n=a or c or g or t

<400> 5

tgngcytcna tytgrrtnac 20

<210> 6

<211>

<212> PRT

<213> Trichosporonoides megachiliensis

<400> 6

Gln Glu Leu Phe Asp Gln Gly

1

5

<210> 7

<211>

<212> PRT

<213> Trichosporonoides megachiliensis

<400> 7

Val Asn Gln Ile Glu Ala His

1

5